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SNP



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☐ 1: AAC83379. Reports structural polypr...[gi:3978527]

BLink, Links

Features Sequence

LOCUS AAC83379_ 1245 aa linear VRL 11-MAY-2000

DEFINITION structural polyprotein [Sindbis virus].

ACCESSION AAC83379

VERSION AAC83379.1 GI:3978527

DBSOURCE locus AF103728 accession AF103728.1

KEYWORDS .

SOURCE Sindbis virus

ORGANISM Sindbis virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 Alphavirus; WEEV complex.

REFERENCE 1 (residues 1 to 1245)

AUTHORS Liang,G.D., Li,L., Zhou,G.L., Fu,S.H., Li,Q.P., Li,F.S., He,H.H.,
 Jin,Q., He,Y., Chen,B.Q. and Hou,Y.D.

TITLE Isolation and complete nucleotide sequence of a Chinese
 Sindbis-like virus

JOURNAL J. Gen. Virol. 81 (Pt 5), 1347-1351 (2000)

PUBMED 10769078

REFERENCE 2 (residues 1 to 1245)

AUTHORS Li,L., Liang,G.D., Zhou,G.L., Fu,S.H., Jin,Q. and Hou,Y.D.

TITLE Direct Submission

JOURNAL Submitted (01-NOV-1998) State Key Laboratory for Molecular Virology
 and Genetic Engineering, Institute of Virology, CAPM, Ying Xin Jie
 100#, Xuan Wu Qu, Beijing 100052, China

COMMENT Method: conceptual translation supplied by author.

FEATURES Location/Qualifiers

source 1..1245
 /organism="Sindbis virus"
 /strain="XJ-160"
 /db_xref="taxon:11034"
 /lab_host="BHK-21"
 /country="China"

Protein 1..1245
 /product="structural polyprotein"

mat_peptide 1..264
 /product="capsid protein"

mat_peptide 265..328
 /product="E3"

mat_peptide 329..751
 /product="E2"

mat_peptide 752..806
 /product="6K"

mat_peptide 807..1245
 /product="E1"

CDS 1..1245
 /coded_by="AF103728.1:7569..11306"

751
 329
 422

ORIGIN

1 mnrqffnmlg rrpfpaptsm wrprrrrrqaa pmparnglas qiqqlttavs alviggaarp
61 qqprprpppr qkkqppkqlp kpkpktqdk kkrqpakpkp gkrqrmalkl eadrlfdvkn
121 engdvighal amegkvmkpl hvkgtidhpv lsklkftkss aydmefaqlp vnmrseafly
181 tsehpegfyn whhgavqysg grftiprgvg grgdsgrpim dnagrvaiv lggadegtrt
241 alsvvtwnsk gktiktspg teewsaapl tamcllgnvs fpcnrppty trepsraldi
301 leenvnhedy dtlldailyg dfsgnrkrsv tgdftltspy lgtcpsyhht epcfspikie
361 qvwdepddtt iriqtsaqfg ydqsgatsvn kyrymsfdqd htvkeggmdd ikistsgpcr
421 rlghkgyfll akcpggdsvt vsivsssstt sctlarkikp kfvgrerydl ppvygkhih
481 ~~mydr~~lket agyitmhrpg phaytsylee asgkiyakpp sgknityeck cgdyktgtvk
541 trteitgcta ikqcwayksd qtkwvfnspd lirhadhaaq gklhlpfrlv pssckvpvah
601 apsvvhgfkhl islqltdthl tllttrrlga npeptsewii gktvrnfsvg rdgleytwgn
661 hdpvrvyage sapgdphgwp heiiqhyyhr hpaytiltvv saavavligl tvaalctcka
721 rrecltpyal apnavvptsi allccirsan aetfsetmsy lwsnsqpfww aqlciplaav
781 vilvrccsccl pfllvvagvy lgkvdayeha ttipnvpkip ykalversgy aplnleitvv
841 ssqvlpstng eyitckftty vpspkvkccg slecqaaha dynckvfggv ypfmwwggaqc
901 fcdsentoms ~~ayv~~klisadcl vtdyaqavnv htaamkvglr ivygnnttsyl dvyvngvtpg
961 tsdklkiag pvssstfpfn hkvvirglv ynydfpeyga mkpgvfgdiq atsltsrdli
1021 astdirllkp svknvhvpyt qaasgfemwk nnsgrplqet apfgckiavn plravdcsyg
1081 nipisidipn aafirisdap lvstvkcevs gctysadfgg matlqyvdr egqcpvhshs
1141 statlqestv hvlekgavtv hfstaspqan fiislcgkkt tcnaeckppa dhivstphki
1201 dqefqtaisk tswswllalf ggasslliig lmiftcsmlt tstrr

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☐ 1: [AAA96973](#). Reports structural polypr...[gi:334113]

BLink, Links

[Features](#) [Sequence](#)

LOCUS AAA96973 1245 aa linear VRL 13-FEB-2003
 DEFINITION structural polyprotein [Ockelbo virus].
 ACCESSION AAA96973
 VERSION AAA96973.1 GI:334113
 DBSOURCE locus SINOCK82 accession M69205.1
 KEYWORDS .
 SOURCE Ockelbo virus
 ORGANISM Ockelbo virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 Alphavirus; WEEV complex.
 REFERENCE 1 (residues 1 to 1245)
 AUTHORS Shirako, Y., Niklasson, B., Dalrymple, J.M., Strauss, E.G. and
 Strauss, J.H.
 TITLE Structure of the Ockelbo virus genome and its relationship to other
 Sindbis viruses
 JOURNAL Virology 182 (2), 753-764 (1991)
 PUBMED [1673813](#)
 FEATURES Location/Qualifiers
 source 1..1245
 /organism="Ockelbo virus"
 /strain="Edsbyn 82-5"
 /isolate="Ockelbo 82"
 /db_xref="taxon:31699"
 Protein 1..1245
 /product="structural polyprotein"
 mat_peptide 1..264
 /product="C"
 mat_peptide 265..328
 /product="E3"
 mat_peptide 329..751
 /product="E2"
 mat_peptide 752..806
 /product="6K"
 mat_peptide 807..1245
 /product="E1"
 CDS 1..1245
 /coded_by="M69205.1:7653..11390"

ORIGIN

```

1  mnrgffnmlg rrpfpaptam wrprrrrqaa pmparnglas qiqqlttavs alvigqatrp
61  qnprprpppr qkkqapkqpp kpkkpqpek kkkqpaktkp gkrqrmalkl eadrlfdvkn
121 edgdvighal amegkvmkpl hvkgtidhpv lsklkftkss aydmefaqlp vnmrseafy
181 tsehpegfyn whhgavqysg grftiprgvg grgdsgripim dngsrvaiv lggadegtrt
241 alsvtwnsk gktikttepeg teewsaapl v tamcllgns fpcnrppty trepsraldi
301 leenvnheay dtllnailrc gssgrskrsv tddftltspy lgtcsychht epcfspikie
361 qvwdeaddnt iriqtsaqfg ydksgaastn kyrymsfeqd htvkegtmdd ikistsgpcr
421 rlsykygyfll akcpvgdsvt vsiassnsat sctmarkikp kfvgrekydl ppvhgkkip

```

 751
 329-
 423

kipce

481 tvydrlkett agyitmhrpg phaytsylee ssgkvyakpp sgknityeck cgdyktgtvt
541 trteitgcta ikqcvayksd qtkwvfnspd lirhadhtaq gklhlpfkli pstcmvpvah
601 apnvihgfkx islqldtdhl tllttrrlga npepttewii gktvrnftvd rdgleyiwn
661 hepvrvyage sapgdphgwp heivqhyyhr hpvytilava saavammigv tvaalcacka
721 rrecltpyal apnaviptsl allccvrsan aetftetmsy fwsnsqpffw vqlciplaav
781 ivlmrccscclpflvvagay lakvdayeha ttvpnpqip ykalveragy aplnleitvm
841 ssevlpstnq eyitckfttv vpspkvkccg slecqpaaaha dytckvfggv ypfmwggaqc
901 fcdsensqms eaayvelsadc atdhaqaikv htaamkvglr ivygnntsfl dvyvngvtpg
961 tskdlkviag piasasftpfd hkvvihrglv ynydfpeyga mkpgvfgdiq atsltskdli
1021 astdirllkp saknvhvpyt qaasgfemwk nnsgrplqet apfgckiavn plravdcsyg
1081 nipisidipn aafirtsdap lvstvkcdvs ectysadfgg matlqyvdr egqcpvhshs
1141 statlqestv hvlekgavtv hfstaspqan fivslcgkkt tcnaeckppa dhivstphkn
1201 dqefqaaisk tswwlalf ggasslliig ltifacsmml tstrr

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 Range: from to Features: ☐ SNP ☒ CDD ☒ MGC ☒ HPRD ☒ STS ☒ tRNA
☐ 1: [AAO33347](#). Reports structural polypr...[gi:28193973]

BLink, Links

Features Sequence

LOCUS AAO33347 ✓ 1239 aa linear VRL 02-FEB-2003
 DEFINITION structural polyprotein precursor [Barmah Forest virus].
 ACCESSION AAO33347
 VERSION AAO33347.1 GI:28193973
 DBSOURCE accession [AF339488.1](#)
 KEYWORDS .
 SOURCE Barmah Forest virus
 ORGANISM [Barmah Forest virus](#)
 Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus.
 REFERENCE 1 (residues 1 to 1239)
 AUTHORS Kinney, R.M. and Pfeffer, M.
 TITLE Nucleotide sequence analyses of the 26S mRNAs of viruses of the genus Alphavirus
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 1239)
 AUTHORS Kinney, R.M. and Pfeffer, M.
 TITLE Direct Submission
 JOURNAL Submitted (23-JAN-2001) Arbovirus Diseases Branch, Centers for Disease Control and Prevention, P.O. Box 2087, Fort Collins, CO 80522, USA
 COMMENT Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..1239
 /organism="Barmah Forest virus"
 /virion
 /strain="BH 2193"
 /db_xref="taxon:11020"
 /country="Australia"
 /note="isolated in 1974; virus passage P7/SM2/BHK21-1"
 Protein 1..1239
 /product="structural polyprotein precursor"
 mat_peptide 1..253
 /product="capsid protein"
 mat_peptide 254..321
 /product="E3 protein"
 mat_peptide 322..742
 /product="E2 envelope glycoprotein"
 mat_peptide 743..800
 /product="6K protein"
 mat_peptide 801..1239
 /product="E1 envelope glycoprotein"
 CDS 1..1239
 /coded_by="AF339488.1:603..4322"

ORIGIN

1 mdfiptqtffy grrwrpavq ryipqpqppa pprrrrgpsq lqqlvaalga lalqpkqkqk

 742
 222
 520

61 raqkkpkktppkpkktqkp kkptqkkksk pgkrmrncmk iendcifpvm ldgkvngyac
121 lvgdkvmkpa hvkgtidnpe lakltfkkss kydlecaqvp vcmksdaskf thekpeghyn
181 whhgavqfsn grftiptgsg kpgdsgrpif dntgkvvaiv lgganegart alsvvtwnkd
241 mvtritpees vewsaaalni talcvtlqnl fpcdappcap ccyekdpagt lrllsdhyyh
301 pkyyelldst' mhcpqgrrpk' rs' vahfeayk atrpyigwca dcglagscps pvsiehvwsd
361 addgvlkiqv smqigiaksn tinhakiryngangvqeaer stlsvsttap cdilatmghf
421 ilarcrpgsqvevslstdpk llcrtpfshk prfigneksp aptghktrip cktyshtdl
481 treeitmhv' pdvpiqglvs ntgksysldp ktktikykct cgetvkegta tnkitlfncd
541 tapkcityav dntvwqynsq yvprsevtv kgkihvpfpl tdstcavsva pepqvtyrlg
601 evefhfhpmyp tlfisirsig kdpshsqewi dtpmsktiqv gaegveyvwg nnnpvrllwaq
661 kssssahgn pisivshyyd lypywtitvl aslgllivis sgfscflcsv artkcltpyq
721 lapgaqlptf iallccaksa radtlldfsy lwtnnqamfw lqlaspvaaf lclsyccrnl
781 accmkiflgi sglcviatqa yehsttmpnq vgipfkalie rpgyaalpls lvvikselvp
841 slvqdyitcn yktvvpspyi kccggaecsh kneadykcsv ftgvypfmwg gaycfcdten
901 smsevyvtr gesceadhai ayqvhtask aqvmisigel nqtdvdfvng dspariqqsk
961 filgpissaw spfdhkvivy rdevynedya pygsgqagrfdiqrsvns tdvyantnlr
1021 lkrpasgnvh vpytqtpsgf sywkkekgvp lnrnapfgci ikvnpvraen cvygnipism
1081 diadahftri despsvslka cevqsctyss dfggvasisy tsnkvgkcai hshsnsatmk
1141 dsvqdvqesg alsiffatss vepnfvvqvc naritchgkc eppkdhipvy aakhndaefp
1201 sisttawqwl ahttsqplti lvvaiivvvv vsivvcarh

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☐ 1: [AAO33325](#). Reports structural polypr...[gi:28193940]

BLink, Links

Features Sequence

LOCUS AAO33325 1245 aa linear VRL 02-FEB-2003
 DEFINITION structural polyprotein precursor [Babanki virus].
 ACCESSION AAO33325
 VERSION AAO33325.1 GI:28193940
 DBSOURCE accession [AF339477.1](#)
 KEYWORDS .
 SOURCE Babanki virus
 ORGANISM Babanki virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 Alphavirus; WEEV complex.
 REFERENCE 1 (residues 1 to 1245)
 AUTHORS Kinney,R.M. and Pfeffer,M.
 TITLE Nucleotide sequence analyses of the 26S mRNAs of viruses of the
 genus Alphavirus
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 1245)
 AUTHORS Kinney,R.M. and Pfeffer,M.
 TITLE Direct Submission
 JOURNAL Submitted (23-JAN-2001) Arbovirus Diseases Branch, Centers for
 Disease Control and Prevention, P.O. Box 2087, Fort Collins, CO
 80522, USA
 COMMENT Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..1245
 /organism="Babanki virus"
 /virion
 /strain="DakAry 251"
 /db_xref="taxon:48540"
 /country="Cameroon"
 /note="isolated in 1969; virus passage P?/SM2/BHK21-1"
 Protein 1..1245
 /product="structural polyprotein precursor"
 mat_peptide 1..264
 /product="capsid protein"
 mat_peptide 265..328
 /product="E3 protein"
 mat_peptide 329..751
 /product="E2 envelope glycoprotein"
 mat_peptide 752..806
 /product="6K protein"
 mat_peptide 807..1245
 /product="E1 envelope glycoprotein"
 CDS 1..1245
 /coded_by="AF339477.1:619..4356"

ORIGIN

1 mnrgffnmfg rrpfpaptam wrprrrrqaa pmparnglas qiqqlttavs alvigqatrp

751
329

422
423

61 qnprprpppr qkkqapkqpp kpkkpktqek kkkqpakpkp gkrqrmalkl eadrlfdvkn
121 edgdvighal amegkvmkpl hvkgtidhpv lsklkftkss aydmefaqlp vnmrseafly
181 tsehpegfyn whhgavqysg grftiprgvg grgdsgrpim dnsgrvvaiv lggadegtrt
241 alsvvtwnsk gktikttepeg teewsaaplv tamcllgns fpcnrppty trepsraldi
301 leenvnheay dtllnailrc gssgrskrstv tddftltspy lgtcsychht epcfspikie
361 qvwdeaddnt iriqtsaqfg ydqsgaastn kyrymsleqd htvkegtmdd ikistsgpcr
421 rlsykygfl akcpggdsvt vsiassnsat sctmarkikp kfvgrekydl ppvhgkkipc
481 tvydrkett agyitmhrpg phaytsylee ssgkvyakpp sgknityecq cgdyktgtvt
541 trteitgcta ikqcavayksd qtkwvfnspd lirhadhtaq gklhlpfkli pstcmvpvah
601 apnvihgfkhl islqltdthl tllttrrlga npepttewii gktvrnftvd rdgleyiwgn
661 hepvrvyaqe sapgdphgwp heivqhyhr hpvytilava savvammigv tvaalcacka
721 rrecltpyal apnaviptsl allccvrsan aetftetmsy lwsnsqpffw vqlciplaav
781 ivlmrccsccl lpflvvagay lakvdayeha ttvpnpqip ykalveragy aplnleitvm
841 ssevlpstnq eyitckfttv vpspkvkccg slecqaaha dytckvfggv ypfmwggaqc
901 fcdsensqms eayvelsadc atdhaqavkv htaamkvglr ivygnntsfl dvyvngvtpg
961 tsdkdlkviag piasftpfh hkvvihrglv ynydfpeyga mkpgafgdiq atsltskdli
1021 astdirllkp saknvhvpvt qaasgfemwk nnsgrplqet apfgckiaavn plravdcsyg
1081 nipisidipn aafirtsdap lvstvkcdvs ectysadfgg matlqyvdr egqcpvhshs
1141 statlqestv hvlekgavtv histaspqan fivslcgkkt tcnaeckppa dhivstphkn
1201 dqefqaaaisk tswwlalf gassllliig lmifacsmml tstrr

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